

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	510	387.3

FIG. 1A

4D5 10 20 30 40 50
 DIVMTQSHKFMSTSVGDRVSTICKASQDVNTAVAWYQQKPGHSPKLLIYSASFRYT
 HU4D5 DIQMTQSPSSLSASVGDRTVITCRASQDVNTAVAWYQQKPKAPKLLIYSASFLES
 HUV_LκI DIQMTQSPSSLSASVGDRTVITCRASQDVSSYLAWYQQKPKAPKLLIYAASSLES

 V_L-CDR1 V_L-CDR2

6639055

4D5 60 70 80 90 100
 GVPDRFTGNRSGTDTFTTISVQAEGLAVYCCQGHYTPPTFGGCTKLEIKRA
 HU4D5 GVPDRFTGNRSGTDTFTTISVQAEGLAVYCCQGHYTPPTFGGCTKLEIKRT
 HUV_LκI GVPDRFTGNRSGTDTFTTISVQAEGLAVYCCQGHYTPPTFGGCTKLEIKRT

 V_L-CDR3

100 90 80 70 60 50 40 30 20 10

2

VH-CDR2

VH-CDR3

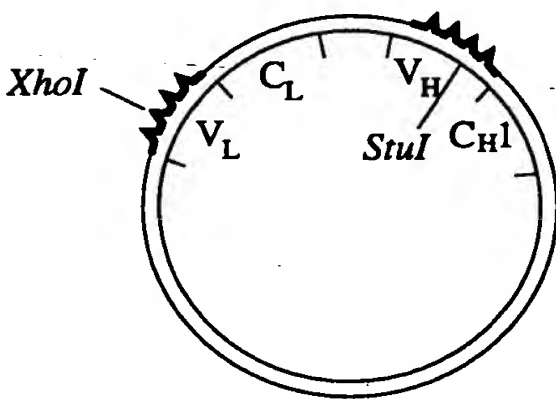
GÖGTLVTVSS

APPROVED	O.G. FIG.	
	CLASS	SUBCLASS
BY	30	3
DRAFTSMAN		

Anneal huV_L or huV_H oligomers to pAK1 template



1. Ligate
2. Isolate assembled oligomers
3. Anneal to pAK1 template (*XhoI*⁻, *StuI*⁺)
4. Extend and ligate



1. Transform *E. coli*
2. Isolate phagemid pool
3. Enrich for huV_L and huV_H (*XhoI*⁺, *StuI*⁻)
4. Sequence verify

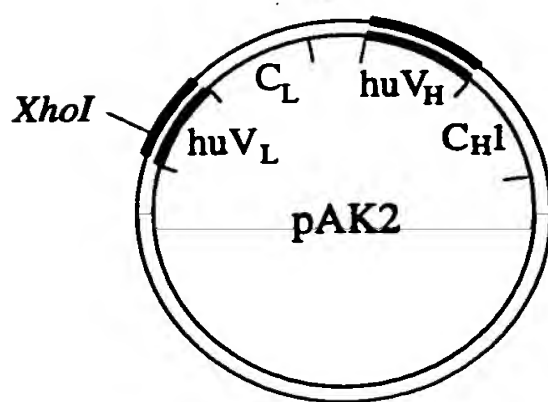


FIG. 2

APPROVED	O.G. FIG.	
	CLASS	SUBCLASS
BY	530	387.3
DRAFTSMAN		

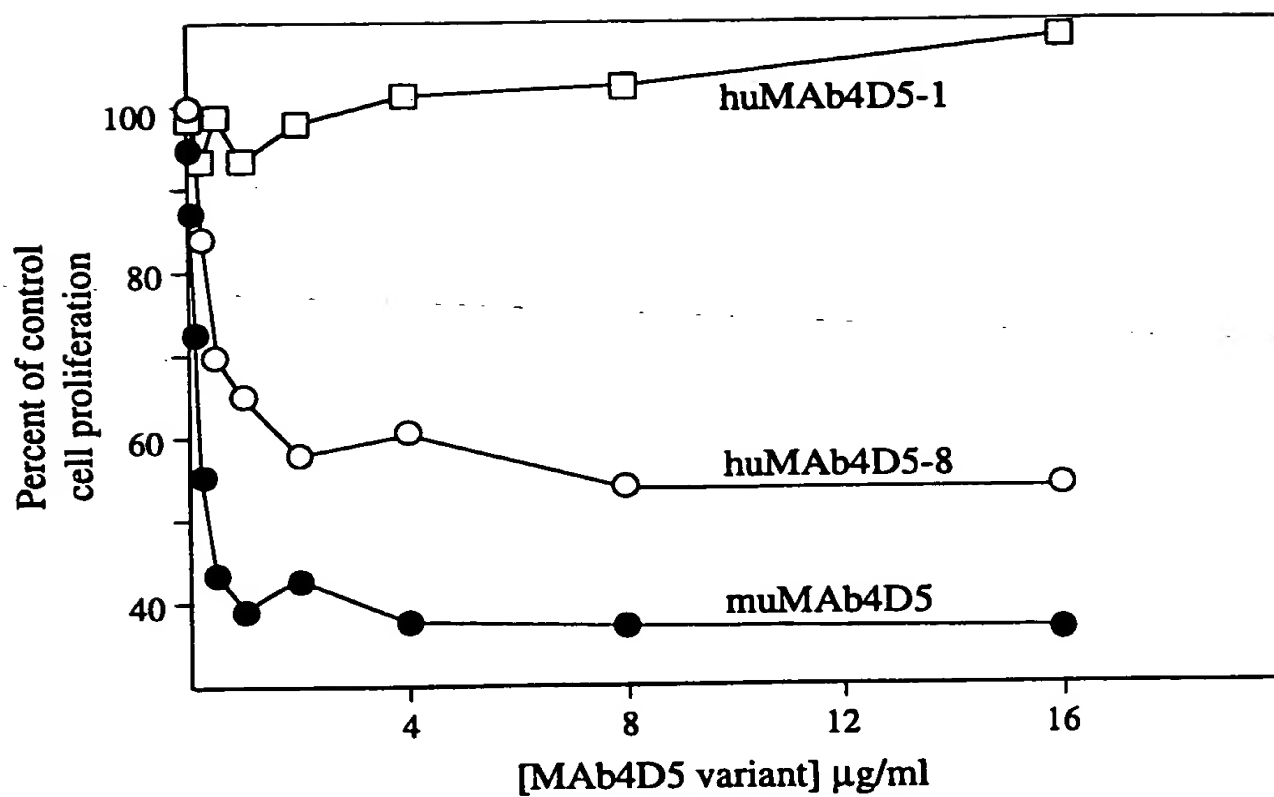


FIG. 3

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	530	387.3

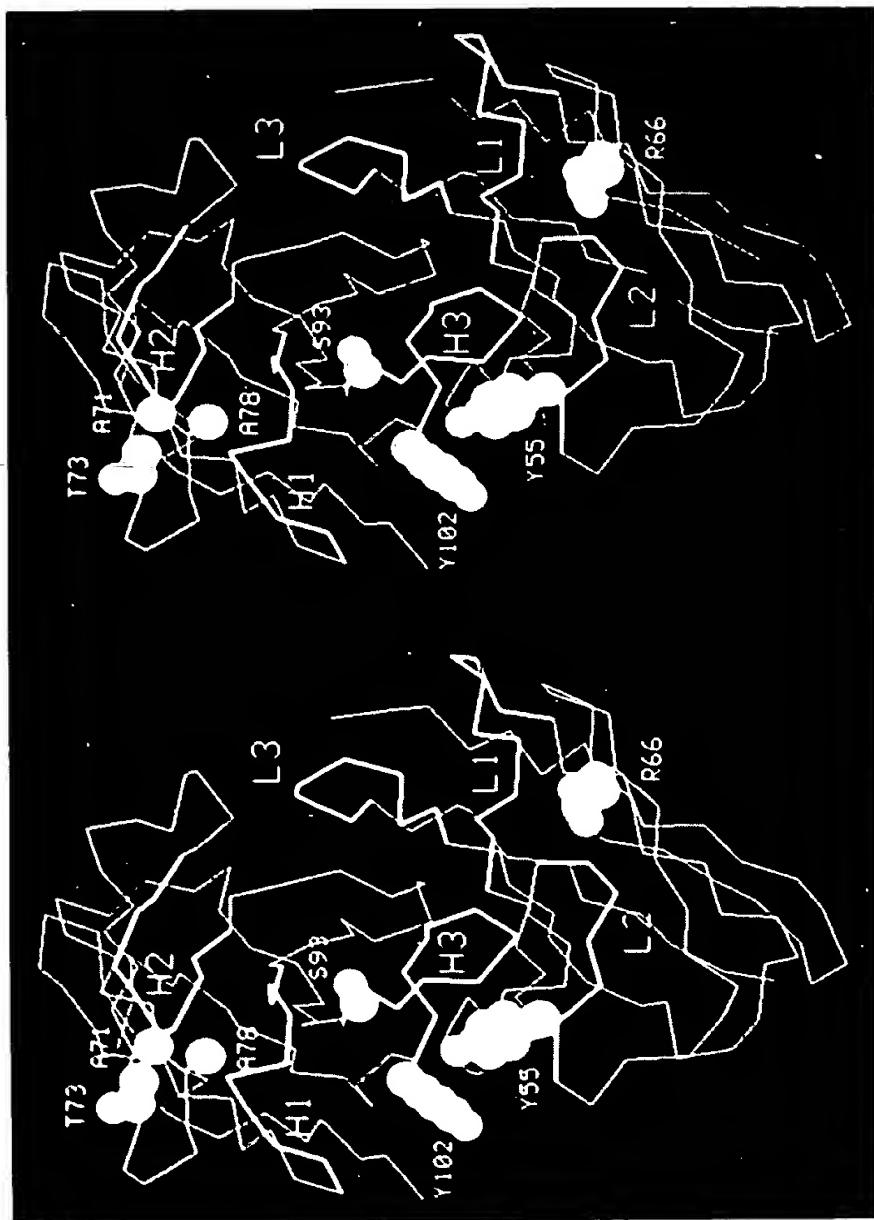


FIG. 4

APPROVED BY	O.G. FIG.	
	CLASS	SUBCLASS
DRAFTSMAN	53a	JP7.3

V_L

	10	20	30	40
muxCD3	DIQMTQT	TSSLSASL	GDRVTIS	CRASQDIRN
huxCD3v1	DIQMTQSP	SSLSASV	GDRVTIT	CRASQDIRN
huκI	DIQMTQSP	SSLSASV	GDRVTIT	CRASQDIRN

NYLNWYQQKP
NYLNWYQQKP
NYLNWYQQKP6
CDR-L1

	50	60	70	80
muxCD3	DGTVKLLI	YYTSLR	LHSGVPS	KFSGSGSG
huxCD3v1	DGTVKLLI	YYTSLR	LHSGVPS	KFSGSGSG
huκI	DGTVKLLI	YYTSLR	LHSGVPS	KFSGSGSG

TDYSLTISNLEQ
TDYSLTISNLEQ
TDYSLTISNLEQ
CDR-L2

	90	100
muxCD3	EDIATYFC	QQGNLTP
huxCD3v1	EDIATYFC	QQGNLTP
huκI	EDIATYFC	QQGNLTP

WTFAGGTKLEIK
WTFAGGTKLEIK
WTFAGGTKLEIK
CDR-L3

V_H

	10	20	30	40
muxCD3	EVQLQQSG	PELVKPG	ASMKISCK	ASGYSFTG
huxCD3v1	EVQLQQSG	PELVKPG	ASMKISCK	ASGYSFTG
huIII	EVQLQQSG	PELVKPG	ASMKISCK	ASGYSFTG

YTMNWVKQS
YTMNWVRQA
YTMNWVRQA
CDR-H1

	50	60	70
muxCD3	HGKNLEWM	GLINPYK	GVSTYNQ
huxCD3v1	HGKNLEWM	GLINPYK	GVSTYNQ
HuIII	HGKNLEWM	GLINPYK	GVSTYNQ

KFDKATLTVDKSSSTAY
KFDKATLTVDKSSSTAY
KFDKATLTVDKSSSTAY
CDR-H2

	80	abc	90	100	abcde	110
muxCD3	MELLSLT	SEDSAV	YYCAR	SGYGD	SDWYFD	VWGAGTT
huxCD3v1	MELLSLT	SEDSAV	YYCAR	SGYGD	SDWYFD	VWGAGTT
huIII	MELLSLT	SEDSAV	YYCAR	SGYGD	SDWYFD	VWGAGTT

TVTVSS
TVTVSS
TVTVSS
DET
CDR-H3

FIG. 5

APPROVED		O.G. FIG.	
BY	CLASS	SUBCLASS	
DRAFTSMAN	530	387.3	

FIG. 6A-1

10 20 30
QVQLQSGPELVKPGASVKISCKTSGYTFTE

H52H4-160
PH52-8.0

MGWSCIILFLVATATGVHSEVQLVESGGGLVQPGGSLRLSCATSGYTFTE
10 20 30 40 50

H52H4-160
PH52-8.0

40 50 60 70 80
YTMHWMKQSHGKSLEWIGGFNPKNGSSHNQRFMDKATLAVDKSTSTAYM

YTMHWMRQAPGKGLEWVAGINPKNGGTSHNQRFMDFRTISVDKSTSTAYM
60 70 80 90 100

H52H4-160
PH52-8.0

90 100 110 120 130
ELRSLTSEDGIIYCARWRGLNGFDVRYFDVWGAGTTVTVSSASTKGPS
..**..*****
QMSLRAEDTAVYYCARWRGLNGFDVRYFDVWGQGTLLTVSSASTKGPS
110 120 130 140 150

H52H4-160
PH52-8.0

140 150 160 170 180
VFPLAPSSKSTSGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL

VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
160 170 180 190 200

H52H4-160
PH52-8.0

190 200 210 220 230
QSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTH

QSSGLYSLSSVTVTSSNFGTQTYTCNVVDHKPSNTKVDKVEPKCC---V
210 220 230 240

H52H4-160
PH52-8.0

240 250 260 270 280
TCPPCPAPPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK

ECPPCPAPP-VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQ
250 260 270 280 290

8

8

8

8

8

8

[illegible]

9

9

**DVQMTQTSSLSASLGDRVTINCRASQDINN
*.***.******.*******

10 20 30 40 50

60 70 80 90 100

110	120	130	140	150
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160 170 180 190 200

210 220 230

210 220 230